

Sup35 →

1 ATGTCGGATTCAAACCAAGGCAACAATCAGCAAAACTACCAGCAATACAGCCAGAACCGTAACCAACAAGGTAAC
1▶ M S D S N Q G N N Q Q N Y Q Q Y S Q N G N Q Q Q G N
79 AACAGATACCAAGGTTATCAAGCTTACAATGCTAAGCCAACCTGCAGGTGGTACTACCAAAATTACCAAGGTTAT
27▶ N R Y Q G Y Q A Y N A Q A Q P A G G Y Y Q N Y Q G Y
157 TCTGGGTACCAACAAGGTTGCTATCAACAGTACAATCCCAGGCCGGTTACCAAGCAACAGTATAATCCTCAAGGAGGC
53▶ S G Y Q Q G G Y Q Q Y N P D A G Y Q Q Q Y N P Q G G
235 TATCAACAGTACAATCCTCAAGGCCGGTTATCAGCAGCAATTCAATCCACAAGGTGGCGTGGAAATTACAAAAACTTC
79▶ Y Q Y N P Q G G Y Q Q Q F N P Q G G R G N Y K N F
313 AACTACAATAACAATTGCAAGGATATCAAGCTGGTTCCAACCACAGTCTCAAGGTATGCTTTGAACGACTTTCAA
105▶ N Y N N N L Q G Y Q A G F Q P Q S Q G M S L N D F Q
391 AAGCAACAAAAGCAGGCCGCTCCAAACCAAAGAAGACTTGAAGCTTGTCTCCAGTCCGGTATCAAGTTGGCAAT
131▶ K Q Q K Q A A P K P K K T L K L V S S S G I K L A N
469 GCTACCAAGAAGGTTGGCACAAACCTGCCAATCTGATAAGAAAGAGGAAGAGAAGTCTGCTGAAACCAAAGAACCA
157▶ A T K K V G T K P A E S D K K E E E K S A E T K E P
547 ACTAAAGAGCAACAAAGGTCGAAGAACCAAGCTTAAAGGAGGAGAACCAAGTCCAGACTGAAGAAAAGACGGAGGAA
183▶ T K E P T K V E E P V K K E E K P V Q T E E K T E E
625 AAATCGGAACCTTCAAAGGTTAGAACCTTAAATCTGAAATCAACACATAATACCAACAAATGCCAATGTTACCAAGT
209▶ K S E L P K V E D L K I S E S T H N T N N A N V T S
← Sup35 GR →
703 GCTGATGCCCTTGATCAAGGAACAGGAAGAACAGTGGATGACGAAGTGTAAACGATCCGGGATGGACTCCAAAGA
235▶ A D A L I K E Q E E V D D E V V N D P R M D S K E
780 ATCCTTAGCTCCCCCTGGTAGAGACGAAGTCCCTGGCAGTTGCTTGGCCAAGGGAGGGGGAGCGTAATGGACTTTA
260▶ S L A P P G R D E V P G S L L G Q G R G S V M D F Y
858 TAAAAGCCTGAGGGGAGGGACTACAGTCAAGGTTCTGCATCTGCCCTCAGTGGCTGCTCTCAGGCCAGATT
286▶ K S L R G G A T V K V S A S S P S V A A A S Q A D S
936 CAAGCAGCAGAGGATTCTCCTTGATTCTCGAAAGGCTCCACAAGCAATGTCAGCAGCAGCAGCAGCAGCA
312▶ K Q Q R I L L D F S K G S T S N V Q Q R Q Q Q Q Q Q
1014 GCAGC
338▶ Q Q Q Q Q Q Q Q Q Q Q Q P G L S K A V S L S M G L
1092 GTATATGGGAGAGACAGAAACAAAGTGTGGGAAATGACTTGGCTACCCACAGCAGGGCAACTTGGCTTTCC
364▶ Y M G E T E T K V M G N D L G Y P Q Q G Q L G L S S
1170 TGGGAAACAGACTTTCGGCTTCTGGAGAAAGCATGCAACCTCAATAGGTGACCCAGCGTCCAGAGAACCCCAA
390▶ G E T D F R L L E E S I A N L N R S T S V P E N P K
1248 GAGTTAACGTCTGCAACTGGGTGTGCTACCCGACAGAGAAGGAGTTCCAAAACACTCACTCGATGCACTTCA
416▶ S S T S A T G C A T P T E K E F P K T H S D A S S E
1326 ACAGCAAAATCGAAAAGCCAGACGGGACCAACGGAGGCAGTGTGAAATGTATCCACAGACCAAGCACCTTGA
442▶ Q Q N R K S Q T G T N G G S V K L Y P T D Q S T F D
1404 CCTCTGAAAGGATTGGAGTTTCCGCTGGGTCCCCAAGTAAAGACACAAACGAGAGTCCCTGGAGATCAGATCTGTT
468▶ L L K D L E F S A G S P S K D T N E S P W R S D L L
1482 GATAGATGAAAACCTTGCTTCTCCCTGGGGAGAGATGATGCCATTCTCTCGAAGGGAACACGAATGAGGATTG
494▶ I D E N L L S P L A G E D D P F L L E G N T N E D C
1560 TAAGCCTTATTTACCGGACACTAAACCTAAATTAGGATACTGGAGATAACATCTTATCAAGTCCCAGCAGTGT
520▶ K P L I L P D T K P K I K D T G D T I L S S P S S V
1638 GGCACCTACCCCAAGTGAACAGAAAAAGATGATTCACTTGTGAACTTGTGACCCCGGGTAATTAGCAAGAGAAA
546▶ A L P Q V K T E K D D F I E L C T P G V I K Q E K L
1716 GGGCCAGTTATGTCAGGCAAGCTTCTGGACAAAATAATTGGTAATAAAATGTCGCAATTCTGTTCTGATGG
572▶ G P V Y C Q A S F S G T N I I G N K M S A I S V H G
1794 TGTGAGTACCTCTGGAGGACAGATGTACCACTATGACATGAATACAGCATCCCTTCAGCAGCAGGATCAGAAC
598▶ V S T S G G Q M Y H Y D M N T A S L S Q Q Q D Q K P
1872 TGTTTTAATGTCATTCCACCAATTCTGTGGTCTGAAAACCTGGAAATAGGTGCCAAGGCTCCGGAGGGACAGCCT
624▶ V F N V I P P I P V G S E N W N R C Q G S G E D S L
1950 GACTTCCTTGGGGCTCTGAACCTCCAGGCCGGTCAGTGTCTTCTAATGGGTACTCAAGCCCTGGAAATGAGACCA
650▶ T S L G A L N F P G R S V F S N G Y S S P G M R P D
2028 TGTAAGCTCTCCATCCAGCTCGTCAGCAGCCACGGGACCCCTCCAAGCTCTGCCCTGGTGTGCTCCGATGAGAC
676▶ V S S P P S S S S A A T G P P P P K L C L V C S D E A
2106 TTCAGGATGTCATTACGGGTGCTGACATGTGAAAGCTGCAAAGTATTCTTAAAGAGGAGCTGGAAGGACAGCACAA
702▶ S G C H Y G V L T C G S C K V F F K R A V E G Q H N

FIG. 1A

2184 TTACCTTGTGCTGGAAGAACGATTGCATCATTGATAAAATTGAGGAAAAACTGCCAGCATGCCGTATCGGAA
728▶ Y L C A G R N D C I I D K I R R K N C P A C R Y R K
2262 ATGCTTCAGGCTGGAATGAACCTTGAGCTCGAAAAACAAAAGAAAAAATCAAAGGGATTCAAGCCACTGCAGG
754▶ C L Q A G M N L E A R K T K K K I K G I Q Q A T A G
2341(GR526)
2340 AGTCTCACAGAACACTTCGAAAATCCTAACAAAACAATAGTCTGCAGCATTACCAACAGCTCACCCCTACCTGGT
780▶ V S Q D T S E N P N K T I V P A A L P Q L T P T L V
2418 GTCACTGCTGGAGGTGATTGAACCCGAGGTGTTGTATGCAGGATATGATAGCTCTGTCAGATTCAAGCATGGAGAAT
806▶ S L L E V I E P E V L Y A G Y D S S V P D S A W R I
2496 TATGACCACACTCAACATGTAGGTGGCGTCAAGTGATTGCAGCAGTGAATGGGCAAAGGCATACTAGGCTTGAG
832▶ M T T L N M L G G R Q V I A A V K W A K A I L G L R
2574 AAACCTACACCTCGATGACCAAATGACCCCTGCTACAGTACTCATGGATGTTCTCATGGCATTTGCCCTGGGTTGGAG
858▶ N L H L D D Q M T L L Q Y S W M F L M A F A L G W R
2652 ATCATACAGACAATCAAGCGAAACCTGCTCTGCTTGTCTGATCTGATTATTAAATGAGCAGAGAATGTCTCTACC
884▶ S Y R Q S S G N L L C F A P D L I I N E Q R M S L P
2730 CTGCATGTATGACCAATGTAACACATGCTGTTGCTCTGAAATTACAAAGATTGCAGGTATCCTATGAAGAGTA
910▶ C M Y D Q C K H M L F V S S E L Q R L Q V S Y E E Y
2808 TCTCTGTATGAAAACCTTACTGCTCTCCTCAGTTCTAAGGAAGGTCTGAAGAGCCAAGAGTTATTGATGAGAT
936▶ L C M K T L L L S S V P K E G L K S Q E L F D E I
2886 TCGAATGACTTATATCAAAGAGCTAGGAAAAGCCATCGTCAAAAGGGAGGGAACTCCAGTCAGAACTGGCAACGGTT
962▶ R M T Y I K E L G K A I V K R E G N S S Q N W Q R F
2964 TTACCAACTGACAAAGCTTCTGGACTCCATGCATGAGGTGGTTGAGAATCTCCCTACCTACTGCTTCCAGACATTITP
988▶ Y Q L T K L L D S M H E V V E N L L T Y C F Q T F L
3042 GGATAAGACCATGAGTATTGAATTCCCAGAGATGTTAGCTGAAATCATCACTAATCAGATACCAAAATATTCAAATGG
1014▶ D K T M S I E F P E M L A E I I T N Q I P K Y S N G
3120 AAATATCAAAAAGCTTCTGTTCATCAAAAATGA
1040▶ N I K K L L F H Q K •

FIG. 1B

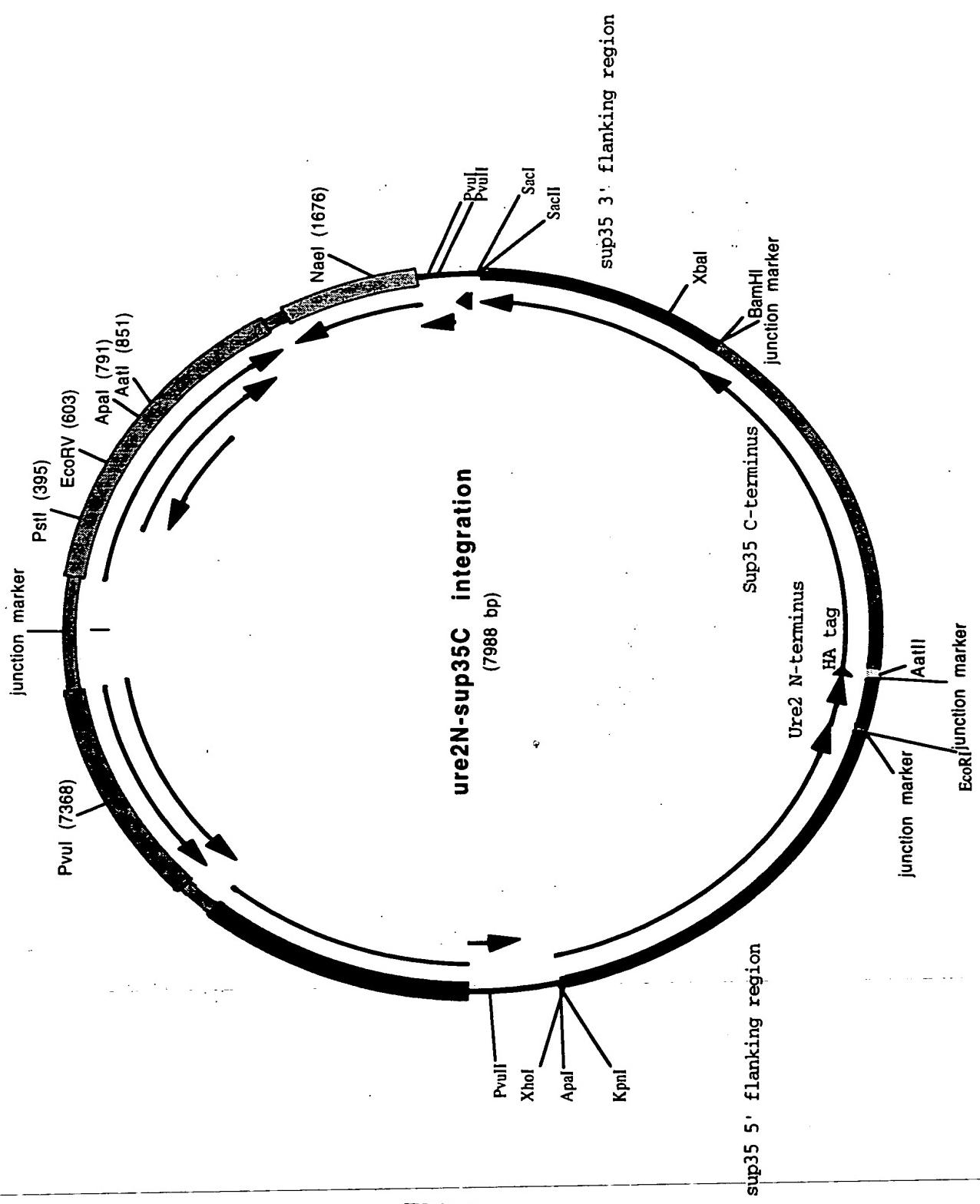


FIG. 2

1 TCGGGGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTGCT GTAGGGAT GCGGGAGCA GACAAGCCG
 0◀ 101 TCAGGGGGC TCAGGGGTG TTGGGGGTG TCGGGGGTGC CTTAACTATG CGGAGATCAGA CGAGATGTA CTGAGAGTC ACCATACAC AGCTTTCAA
 201 TTCAATTCA CATTTTTT TTATTCTTTT TTTCGATTTC GGTCTCTTGT AAATTTTTT GATTGGTAA TCTCGAACAA GAAGGAAGA CGAAGGAAGG
 301 AGCACAGACT TAGATTGGTA TATATACGCA TATCTAGTGT TGAGAAACA TCAAATTGCC CAGTATCTT AACCCAACTG CACAGAACAA AAAACCTGAG
 401 GAAACGAAGA TAAATCATGT CGAAAGCTAC ATATAAGGAA CGTGTGCTA CTGATCCTAG TCCCTGTCT GCCAAGCTAT TTAATATCAT GCACGAAAG
 PsII (395)
 501 CAAACAACT TGTGTGCTTC ATTGGATGTT CGTACCAACCA AGGAATTACT GGAGTGTAGTT GAAGGATTAG GTCCCAAAAT TTGTTTACTA AAAACACATG
 29▶ Q T N L C A S L D V R T T K E L L E L V E A L G P K I C L L K T H
 142◀ C V F K H A E N S T R V V L S N S S N T S A N P G L I Q K S F V C T
 EcoRV (603)
 601 TGGATATCTT GACTGATTTC TCCATGGAGG GCACAGTTA GCAAGTACAA TTTTTTACTC TTICGAAGACAA GAAAATTTGC
 62▶ V D I L T D F S M E G T V K P L K A L S A K Y N F L L F E D R K F A
 109◀ S I K V S K E M S P V T L G S F A N D A L Y L K K S K S S L F N A
 Apal (791)
 701 TGACATGGT AATACAGTCA AATTGCGATPA CTCTGGGGT GTATACAGAA TAGCAGAATG GGAGACATT ACGAATGCAC ACGGTGTGGT GGGCCAGGT
 95▶ D I G N T V K L Q Y S A G V Y R I A E W A D I T N A H G V V G P G
 76◀ S M P L V T L N C Y E A P T Y L I A S H A S M V F A C P T T P G P
 AaiI (851)
 801 ATTGGTAGCG GTITGAAGCA GGGGGAGAA GAAGTACAA AGGAACCTAG AGGCCCTTGT ATGTTAGCAG AATGTCATG CAAGGGCTCC CTATCTACTG
 129▶ I V S G L K Q A A E E V T K E P R G L L M L A E L S C K G S L S T
 42◀ I T L P K F C A A A S S T V F S G L P R K I N A S N D H L P E R D V P
 901 GAGAATATAC TAAGGGTACT GTGACATTC CGAAGAGCGA CAAAGATTT GTTATCGCTT TTATTCATCA AAGAGACATG GGTGGAAAGAG ATGAAAGGTAA
 162▶ G E Y T K G T V D I A K S D K D F V I G F I A Q R D M G G R D E G Y
 9◀ S Y V L P V T S M
 1001 CGATTGGTTG ATTATGACAC CCGGTGTGGG TTAGATGAC AAGGGAGACG CATTGGTCA ACAGTATAGA ACCGTGGATG ATGTGGTCTC TACAGGATCT
 195▶ D W L I M T P G V G L D D K G D A L G Q Q Y R T V D D V V S T G S
 1101 GACATTATTA TTGTTGGAG AGGACTATTG GCAAGGGAA CGGTAGGGTAA GGATGCTTACA GAACTGTTACA GAAAGCAGG CITGGAAAGCA TATTGAGAA
 229▶ D I I V G R G L F A K G R D A K V E G E R Y R K A G W E A Y L R

FIG. 3A

FIG. 3B

Sequence alignment diagram showing DNA strands 3231, 3455, 3679, 3791, 3903, 4015, 4127, 4239, 4351, 4463, 4575, 4687, 4799, 4911, 5023, 5135, and 5247. The diagram highlights a junction marker at position 4127 and an EcoRI junction mark at position 4239. Arrows indicate the direction of reading for each strand.

FIG. 3C

5359 ACTTGTAAACGGGTCAGGTATTGGGGAAAGGGCCTTGTAGGTCACCGGAAGGATTTGGCTAATGGGGCTCGACGATTCCCTCAGTCAGTCAAAGGTTTTCTT
 5471 TGTGGTTGCCAGCTTCCCTTGGGGCTTCAGACTTATCCCTCTTATCCCTTCCCTGGTATTGCTTCAATTCTGGTCAAGTCTCAGTG
 5583 TTCAATATGTTGAAACACCTATTAACGGGTTAACGTTAAACTGTTAACGTTAACATGGCTTATTACATTGCTTAAATGATGATATCTT
 Xhol Apal KpnI
 5695 C TCGAGGGGG GCCCGGTACC CAGGTTTGT TCCCTTAGT GAGGTTAAT TCCGAGCTTG GCGTAATCAT GGTCATAGCT GTTTCCTGT TGAAATTGTT
 5796 ATCCGTCAC AATTCCACAC AACATACGAG CGGAAGCAT AAAGTGTAAA GCCTGGGGTG CCTAATGAGT GAGGTAACTC ACATTAATG CGTTGGCTC
 ↓
 Pvull
 5896 ACTGCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA TCGGCCAAGC TCAAGCTCAC TCAAAGGGT TAATACGGTT TCAGGGATA
 5996 TCCTCGCTCA CTGACTCGCT GGCCTCGGT GTCGGCTGC GGGGAGGGT ATCCAGCTCAC TCAAAGGGG TAATACGGG TAATACGGTT TCAGGGATA
 6096 ACGCAGAAA GAACATGTGA GCAAAAGGCC AGCAAAAGGC CAGGAACCGT AAAAAGGGCG CGTTGCTGCC GTTTTCCAT AGGCTCCGCC CCCCTGACGA
 6196 GCATCACAAA AATGAGCAGT CAAGTCAGAG GTGGGAAAC CCGACAGGAC TATAAAGATA CCAGGGTTT CCCCCGGAA GCTCCCTGT GGCCTCTCCT
 6296 GTTCCGACCC TGCCGCTTAC CGGATAACCTG TCCGCCTTC TCCCCTCGG AAGCGTGGG CTTTCTCATTA GCTCACCGCT TAGGTATCTC AGTTCGGTGT
 6396 AGTCGGTTCG CTCCAAGCTG GGCTGTGTGC ACGAACCCC CGTTCAGGCC GACCGCTGCC CCTTATCCG TAACTATCGT CTTCAGTCAC ACCCGTAAG
 6496 ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGGGTGCT ACAGAGTCTC TGAAGTGTGC GCCTAATAC
 6596 GGCTACACTA GAAGGACAGT ATTGGGTATC TGGCTCTGC TGAAGGCCAGT TACCTTCGGA AAAAGAGCTG GTAGGCTCTG ATCCGGAAA CAAACACCG
 6696 CTGGTAGGGG TGTTTTTTT GTTGCAGGC AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTT TCTACGGGGT CTGACGCTCA
 6796 GTGGAACGAA AACTCACGTT AAGGGATT TTGTATGAGA TTATCAAAAA GGATCTTCAC CTAGATCTT TAAATTAAA ATGAAAGTT TAAATCAATC
 6896 TAAAGTATAT ATGAGTAAAC TTGGCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGCTTATT TGTTCATCC ATAGTGCT
 6996 GACTCCCCGT CGTGTAGATA ACTACGATA GGGAGGGCTT ACCATCTGGC CCCAGTGTG CAATGATACC GCGAGACCCA CGTCACCGG CTCCAGATT
 2644 S G T T Y I V V I R S P K G D P G L A A I I Q R N R E D M T A Q
 7096 ATCAGCAATA AACCAAGCCAG CGGGAAAGGGC CGAGGGCAGA AGTGGTCTG CAACTTATC CGCCTCCATC CAGTCATTA ATTGTTGCCG GGAAGCTAGA
 2314 D A I F W G A P L A S R L P G A V K D A E M W D I L Q Q R S A L

FIG. 3D

7196	GTAAGTAGTT CGCCAGTAA TAGTTGCGC AACGTGTTG CCATTGCTAC AGGCATGTC CCGTACAGCT GTCGTTGG TATGGCTCA TTACGCTCCG	
1974	T L L E G T L L K R L T T A M A V P M T T D R E D N P I A E N L E P	PvuI (7368)
7296	GTTCCCAACG ATCAAGGGCA GTTACATGAT CCCCATGTT GTGCCAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGT GTTCAGAGTA AGTTCGGC	
1644	E W R D L R T V H D G M N H L F A T L E K P G G I T T L L N A A	
7396	AGTGTATCA CTCTATGGTAA TGCCAGCACT GCATAATTCGTTA TGCCATCGT AAATGCTTT TCTGTGACTG GTGAGTACTC ACCAAAGTCA	
1314	T N D S M T I A A S C L E R V T M G D T L H K E T V P S Y E V L D	
7496	TTCTGAGAAT AGCTGATCGC GCGACCAGT TGCTCTTGCC CGGGCTCAT ATGGGATAAT ACCGGCCAC ATTAGCAGAAC TTAAAGTG CTCTATCATTG	
974	N Q S Y H I R R G L Q E Q G A D I R S L V A G C L L V K F T S M M P	
7596	GAAAACGTC TTGGGGCGGA AAACCTCTAA GGATCTTACG GCTGTGAGA TCCAGTTCGA TGTAACCCAC TCGTGACCCC AACTGATCTT CAGCATCTT	
644	F R E E P R F S E L I K G S N L D L E I Y G V R A G L Q D E A D K	
7696	TACTTCACC AGCGTTCTG GGTGAGCAA AACAGGAAGG CAAATGGGG CAAAAAGGG AATAAGGGG ACACGGAAAT GTTGAATACT CATACTCTC	
314	V K V L T E P H A F V P L C F A A F F P I L A V R F H Q I S M	
7796	CTTTCAAT ATTATGAA CATTATCAG GTTATGTC TCATGAGGG ATACATT GAATGTATT AGAAAATAA ACAATAGGG GTTCGGCGCA junction man	
7896	CATTTCGG AAAAGTGCC CCTGACGTCT ATAAACCT TAATPATCATG ACATPAACCT ATAAATAG GCGTATCACG AGGCCTTTC GTC	

FIG. 3E

Spontaneous conversion of Sup35 repeat mutants

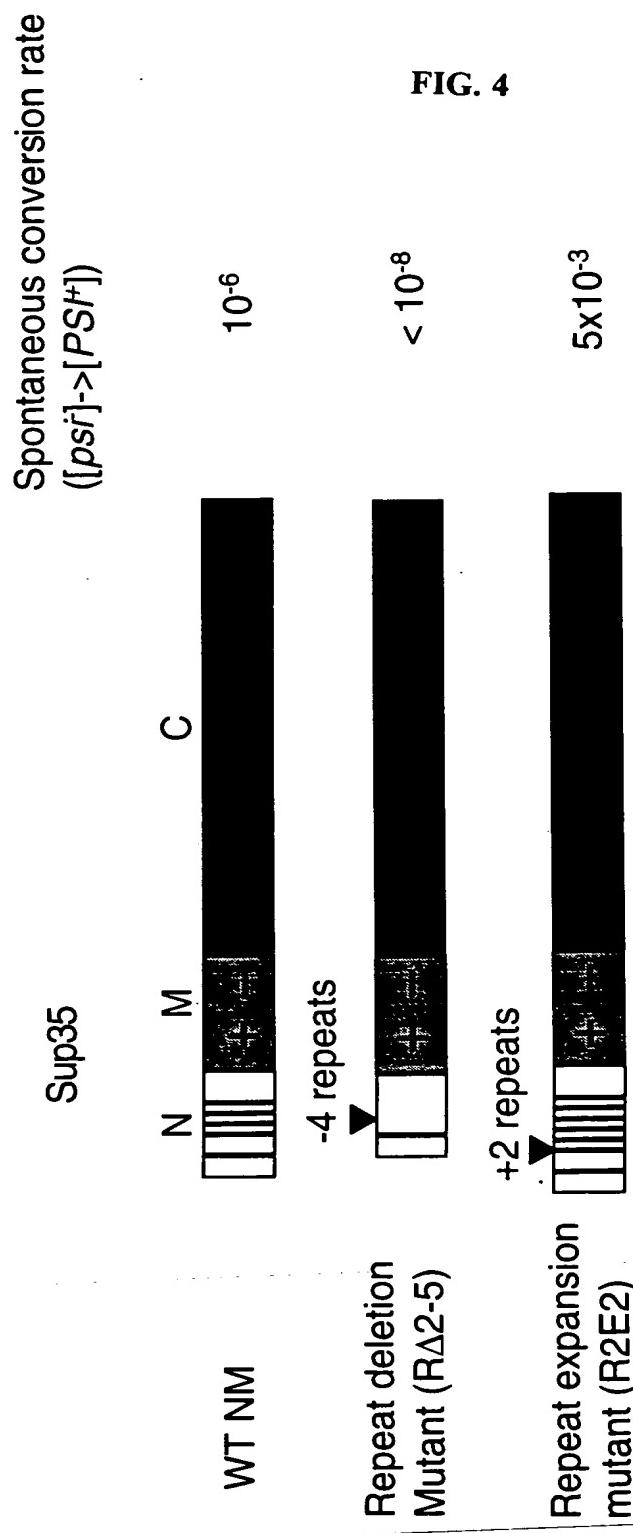


FIG. 4